Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims:

1–50. (Cancelled).

51. (New) A universal gel system for analyzing a sample, the system comprising:
a capture probe comprising nucleic acid, the capture probe being covalently attached to an electrophoretic medium; and
a linking member comprising nucleic acid and comprising
(i) a first region comprising a first nucleic acid sequence substantially complementary to a region of the capture probe, and
(ii) a second region comprising a second nucleic acid sequence for binding to a region of a target molecule in the sample, wherein the first nucleic acid sequence is substantially absent from the sample to be analyzed.

52. (New) The system of claim 51 wherein the linking member comprises at least one of DNA, PNA, or 2-O-methyl RNA.

53. (New) The system of claim 51 wherein the capture probe comprises at least one of DNA, RNA, PNA, or 2-O-methyl RNA.

54. (New) The system of claim 51 wherein the capture probe comprises a nucleic acid sequence of about 8 nucleotides to about 50 nucleotides in length.

55. (New) The system of claim 51 wherein the nucleic acid capture probe comprises a nucleic acid sequence of about 15 nucleotides to about 25 nucleotides in length.

56. (New) The system of claim 51 wherein the linking member comprises a detectable moiety.

57. (New) The system of claim 51 wherein the target molecule comprises a detectable moiety.

58. (New) The system of claim 51 wherein the system comprises a plurality of capture probes arranged in a layer.

59. (New) The system of claim 58 wherein the plurality of capture probes are the same.

60. (New) The system of claim 51 wherein the electrophoretic medium comprises a layer and the system further comprises a second layer comprising an electrophoretic medium.

61. (New) A method for analyzing a sample, the method comprising the steps of:

(a) contacting a sample with a linking member comprising nucleic acid and comprising (i) a first region comprising a first nucleic acid sequence substantially complementary to a region of a capture probe, and (ii) a second region comprising a second nucleic acid sequence for binding to a region of a target molecule in the sample to form a linking member/target complex comprising the linking member bound to the target molecule wherein the first nucleic acid sequence is substantially absent from the sample to be analyzed; and

(b) contacting the linking member with the capture probe, the capture probe covalently attached to an electrophoretic medium.

62. (New) The method of claim 61 wherein the contacting step occurs in solution.

63. (New) The method of claim 61 further comprising the step of detecting at least one of the target molecule and the linking member.

64. (New) The method of claim 61 further comprising the step of electrophoretically migrating the linking member/target complex through the electrophoretic medium.

65. (New) The method of claim 61 wherein the sample comprises nucleic acid.

66. (New) The method of claim 61 wherein the sample comprises SRP RNA from a non-viral organism.

67. (New) The method of claim 66 wherein the SRP RNA comprises 4.5S RNA.

68. (New) The method of claim 61 wherein the linking member comprises a detectable moiety.

69. (New) The method of claim 61 wherein the target molecule comprises a detectable moiety.

70. (New) The method of claim 61 further comprising contacting the target molecule with a signal probe comprising a detectable moiety.